AMENDMENTS TO THE SPECIFICATION

On pages 7-8, please replace the paragraph bridging Pages 7-8 with the following amended paragraph:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. The NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See ~~http://www.ncbi.nlm.nih.gov~~ www.ncbi.nlm.nih.gov.

On page 24, please replace the second full paragraph with the following amended paragraph:

Two groups of APIs are described herein by the amino acid sequencing of AFs. APIs were isolated, subjected to proteolysis, and analyzed by mass spectrometry using in this instance the methods and apparatus of the Preferred Technology, it being understood that the preferred technology is set forth as representative but not restrictive of the invention. One skilled in the art can identify sequence information from proteins analyzed by mass spectrometry and/or tandem mass spectrometry using various spectral interpretation methods and database searching tools. Examples of some of these methods and tools can be found at the Swiss Institute of Bioinformatics web site at ~~http://www.expasy.ch/~~ www.expasy.ch/, and the European Molecular Biology Laboratory web site at www.mann.embl-heidelberg.de/Services/PeptideSearch/.

Identification of APIs was performed using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989) with uninterpreted tandem mass spectra of tryptic digest peptides as described in the Examples, infra.

On page 54, please replace the second full paragraph with the following amended paragraph:

In Tables IV and V above, some APIs disclosed herein correspond to isoforms of previously identified proteins encoded by genes whose sequences are publicly known. To screen such a gene, any probe may be used that is complementary to the gene or its complement; preferably the probe is 10 nucleotides or longer, more preferably 15 nucleotides or longer. The SWISS-PROT and trEMBL databases (held by the Swiss Institute of Bioinformatics (SIB) and the European Bioinformatics Institute (EBI) which are available at ~~http://www.expasy.ch/~~ www.expasy.ch/) and the GenBank database (held by the National Institute of Health (NIH) which is available at ~~http://www.ncbi.nlm.nih.gov/~~ www.ncbi.nlm.nih.gov/) provide protein sequences comprising the amino acid sequences listed for the APIs in Tables IV and V under the following accession numbers and each sequence is incorporated herein by reference:

On page 64, please replace the first full paragraph with the following amended paragraph:

As used herein "tryptic digest peptides" are peptides produced through treatment of the protein with the enzyme trypsin. Trypsin cleaves specifically at the carboxyl side of lysine (Lys) and arginine (Arg) residues, so that the tryptic digest peptides generated should have a Lys or Arg as the C-terminal amino acid, unless the peptide fragment was obtained from the C-terminal of the protein. Similarly, the amino acid directly preceding the N-terminal amino acid of the tryptic digest peptides should also be a Lys or Arg, unless the peptide was obtained from the N-terminal of the protein. The mass of a tryptic digest peptide corresponds to the total mass of the constituent amino acid residues of the peptide with the addition of a water molecule (H_2O). As used herein, the "partial sequence" is an amino acid sequence within the tryptic digest peptide determined from the interpretation of the tandem mass spectrum of the peptide. As used herein, the "N-terminal mass" is the mass measured by mass spectrometry (having an error of measurement of approximately 100 parts-per-million or less) of the portion of the tryptic digest peptide extending from the start of the partial sequence to the N-terminus of the peptide. This is a

neutral mass corresponding to the total mass of the constituent amino acid residues extending from the partial sequence to the N-terminus of the peptide. As used herein, the "C-terminal mass" is the mass measured by mass spectrometry (having an error of measurement of approximately 100 parts-per-million or less) of the portion of the tryptic digest peptide extending from the end of the partial sequence to the C-terminus of the peptide. This mass corresponds to the total mass of the constituent amino acid residues extending from the end of the partial sequence to the C-terminus of the peptide with the addition of a water molecular (H_2O), and a single proton (H^+). In Table IX, supra, the preferred and degenerate sets of probes are described using GCG Nucleotide Ambiguity Codes as employed in GCG ~~SeqWeb™~~ SEQWEB™ sequence analysis software (~~SeqWeb™~~ SEQWEB™ version 1.1, part of Wisconsin Package Version 10, Genetics Computer Group, Inc.). These Nucleotide Ambiguity Codes have the following meaning:

On page 66, please replace the second full paragraph with the following amended paragraph:

Alternatively, the anti-API antibodies can be nonspecifically immobilized to a suitable support, such as silica or ~~Celite®~~ CELITE® resin. This material is then used to adsorb to bacterial colonies expressing the API protein or API-related polypeptide as described herein.

On pages 66-67, please replace the paragraph bridging pages 66-67 with the following amended paragraph:

PCR can be carried out, e.g., by use of a Perkin-Elmer Cetus thermal cycler and Taq polymerase (~~Gene Amp®~~ GENE AMP® or AmpliTaq DNA polymerase). One can choose to synthesize several different degenerate primers, for use in the PCR reactions. It is also possible to vary the stringency of hybridization conditions used in priming the PCR reactions, to allow for greater or lesser degrees of nucleotide sequence similarity between the degenerate primers and the corresponding sequences in the DNA. After successful amplification of a segment of the sequence encoding an API, that segment may be molecularly cloned and sequenced, and utilized as a probe to isolate a complete genomic clone. This, in turn, will permit the determination of the gene's complete nucleotide sequence, the analysis of its expression, and the production of its protein product for functional analysis, as described infra.

On pages 75-76, please replace the paragraph bridging pages 75-76 with the following amended paragraph:

Domains of some of the APIs provided by the present invention are known in the art and have been described in the scientific literature. Moreover, domains of an API can be identified using techniques known to those of skill in the art. For example, one or more domains of an API can be identified by using one or more of the following programs: ProDom, TMpred, and SAPS. ProDom compares the amino acid sequence of a polypeptide to a database of compiled domains (see, e.g., ~~http://www.toulouse.inra.fr/prodom.html~~ www.toulouse.inra.fr/prodom.html; Corpet F., Gouzy J. & Kahn D., 1999, Nucleic Acids Res., 27:263-267). TMpred predicts membrane-spanning regions of a polypeptide and their orientation. This program uses an algorithm that is based on the statistical analysis of TMbase, a database of naturally occuring transmembrane proteins (see, e.g., ~~http://www.ch.embnet.org/software/TMPRED_form.html~~ www.ch.embnet.org/software/TMPRED_form.html; Hofmann & Stoffel. (1993) "TMbase--A database of membrane spanning proteins segments." Biol. Chem. Hoppe-Seyler 347,166). The SAPS program analyzes polypeptides for statistically significant features like charge-clusters, repeats, hydrophobic regions, compositional domains (see, e.g., Brendel et al., 1992, Proc. Natl. Acad. Sci. USA 89: 2002-2006). Thus, based on the present description, those skilled in the art can identify domains of an API having enzymatic or binding activity, and further can identify nucleotide sequences encoding such domains. These nucleotide sequences can then be used for recombinant expression of an API fragment that retains the enzymatic or binding activity of the API.

On page 98, please replace Table X with the following amended table:

API	References
API-39, API-44, API-178, API-188	Structural Biology 7, 312-321, 2000 J. Am. Chem. Soc. 122, 2178-2192, 2000
API-76 API-78 API-79	Clin Chem 1993 Feb 39:2 309-12 J Immunol Methods 1987 Aug 24 102:1 7-14

API-80 API-82 API-140	
API-38 API-74 API-105 API-124 API-130 API-138 API-169 API-172	J Clin Lab Immunol 1986 Dec 21:4 201-7
API-123 API-126	Neuroendocrinology 1992 Mar 55:3 308-16
API-186	J Chromatogr 1991 Jul 5 567:2 369-80; Clin Chem 1989 Apr 35:4 582-6
API-52	J Chromatogr 1987 Dec 18 411:498-501 Eisei Shikenjo Hokoku 1972 90: 89-92 Analyst 1990 Aug 115:8 1143-4
API-182	Biochem J 1997 Mar 1 322 (Pt 2): 455-60; Biochem Soc Trans 1997 Nov 25:4 S591; Biochim Biophys Acta 1986 Oct 10 888:3 325-31 ~~http://www.promega.com~~ www.promega.com

On page 125, please replace the second full paragraph with the following amended paragraph:

The gels were cast between two glass plates of the following dimensions: 23 cm wide x 24 cm long (back plate); 23 cm wide x 24 cm long with a 2 cm deep notch in the central 19 cm (front plate). To promote covalent attachment of SDS-PAGE gels, the back plate was treated with a 0.4% solution of y-methacryl-oxypropyltrimethoxysilane in ethanol (~~BindSilane~~ BINDSILANE; Pharmacia Cat. # 17-1330-01). The front plate was treated with (~~RepelSilane~~™ REPELSILANE™ Pharmacia Cat. # 17-1332-01) to reduce adhesion of the gel. Excess reagent

was removed by washing with water, and the plates were allowed to dry. At this stage, both as identification for the gel, and as a marker to identify the coated face of the plate, an adhesive bar-code was attached to the back plate in a position such that it would not come into contact with the gel matrix.

On pages 134-135, please replace the paragraph bridging pages 134-135 with the following amended paragraph:

Proteins in AFs were robotically excised and processed to generate tryptic digest peptides. Tryptic peptides were analyzed by mass spectrometry using a PerSeptive Biosystems ~~Voyager-DE~~™ VOYAGER-DE™ STR Matrix-Assisted Laser Desorption Ionization Time-of-Flight (MALDI-TOF) mass spectrometer, and selected tryptic peptides were analyzed by tandem mass spectrometry (MS/MS) using a Micromass Quadrupole Time-of-Flight (Q-TOF) mass spectrometer (Micromass, Altrincham, U.K.) equipped with a ~~Nanoflow~~™ NANOFLOW™ electrospray Z-spray source. For partial amino acid sequencing and identification of APIs uninterpreted tandem mass spectra of tryptic peptides were searched using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989), version v.C.1. Criteria for database identification included: the cleavage specificity of trypsin; the detection of a suite of a, b and y ions in peptides returned from the database, and a mass increment for all Cys residues to account for carbamidomethylation. The database searched was database constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI) which is accessible at ~~http://www.ncbi.nlm.nih.gov/~~ www.ncbi.nlm.nih.gov/. Following identification of proteins through spectral-spectral correlation using the SEQUEST program, masses detected in MALDI-TOF mass spectra were assigned to tryptic digest peptides within the proteins identified. In cases where no proteins could be identified through searching with uninterpreted MS/MS spectra of tryptic digest peptides using the SEQUEST program, tandem mass spectra of the peptides were interpreted manually, using methods known in the art. (In the case of interpretation of low-energy fragmentation mass spectra of peptide ions see Gaskell et al., 1992, Rapid Commun. Mass Spectrom. 6:658-662).